What is claim d is:

1. A method for identifying differentially expressed nucleic acids between two samples, comprising:
   a. selecting a first and second nucleic acid sample, wherein the nucleic acid samples contain a repertoire of nucleic acids;
   b. performing reciprocal subtraction between the nucleic acid samples to produce two subtracted nucleic acid samples;
   c. amplifying the two subtracted nucleic acid samples; and
   d. comparing the two subtracted nucleic acid samples to identify differentially expressed nucleic acids.

2. A method for identifying differentially expressed nucleic acids between two samples, comprising:
   a. selecting a first and second nucleic acid sample, wherein the nucleic acid samples contain a repertoire of nucleic acids;
   b. amplifying the two nucleic acid samples;
   c. performing reciprocal subtraction between the amplified nucleic acid samples to produce two subtracted nucleic acid samples; and
   d. comparing the two subtracted nucleic acid samples to identify differentially expressed nucleic acids.

3. The method of claim 2, wherein the two subtracted nucleic acid samples from step c are amplified prior to the comparing of step d.

4. The method of claim 1 or 2, wherein the each of the nucleic acid samples comprises a library of nucleic acids.

5. The method of claim 1 or 2, wherein the nucleic acid samples are mRNA or cDNA derived from mRNA.

6. The method of claim 1 or 2, wherein the nucleic acid samples are obtained from total RNA from E11 and E11-NMT cells.

7. The method of claim 1 or 2, wherein the first and second nucleic acid samples are obtained from cells that differ in their exposure to external factors or in their gene expression.

8. The method of claim 1 or 2, wherein the first and second nucleic acid samples are obtained from cells in different developmental stages.

9. The method of claim 1 or 2, wherein the amplifying of step (d) comprises PCR amplification.

10. The method of claim 9, wherein the PCR amplification uses a set of random primers.

11. The method of claim 9, wherein the 3' primer used in the PCR amplification is a single anchor oligo dT 3' primer.

12. The method of claim 9, wherein the 5' primer is an arbitrary primer.

13. The method of claim 1 or 2, wherein the comparing of step (e) comprises using a gel to separate the nucleic acids from both of the libraries.

14. The method of claim 1 or 2, further comprising PCR amplifying the first and second nucleic acid samples.

15. The method of claim 1 or 2, further comprising reamplifying differentially expressed nucleic acids.

16. The method of claim 1 or 2, wherein the comparing of step (e) comprises comparing the quantities of the two amplified differentially expressed nucleic acids.

17. The method of claim 1 or 2, wherein differences in the quantities of nucleic acid between the two subtracted libraries are electronically quantified.

18. The method of claim 1 or 2, wherein the libraries of step (b) are constructed with λ-ZAP cDNA library kits.

19. The isolated nucleic acid identified by the method of claim 1 or 2, wherein the nucleic acid was not previously known.

20. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PSGen 12.

21. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PSGen 13.

22. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PSGen 23.

23. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PSGen 24.

24. The isolated nucleic acid of claim 19, wherein the

isolated nucleic acid is the nucleic acid designated PSGen 25.

25. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PSGen 26.

26. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PSGen 27.

27. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PSGen 28.

28. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PSGen 29.

29. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PEGen 13.

30. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PEGen 14.

31. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PEGen 15.

32. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PEGen 24.

33. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated

PEGen 28.

34. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PEGen 32.

35. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PEGen 42.

36. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PEGen 43.

37. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PEGen 44.

38. The isolated nucleic acid of claim 19, wherein the isolated nucleic acid is the nucleic acid designated PEGen 48.

39. The isolated nucleic acid molecule of claim 19 which comprises:

(a) one of the nucleic acid sequences as set forth in Figure 35;

(b) a sequence being degenerated to a sequence of (a) as a result of the genetic code;

(c) a sequence encoding one of the amino acid sequences as set forth in Figure 35.

(d) a sequence of at least 12 nucleotides capable of specifically hybridizing to the sequence of (a), (b) or (c)

40. A purified polypeptide comprising one of the amino acid sequence as set forth in Figure 35.